



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Reed, John

(ii) TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LONG, ALDRIDGE & NORMAN LLP

(B) STREET: Suite 600, 701 Pennsylvania Avenue, N.W.

(C) CITY: Washington

(D) STATE: District of Columbia

(E) COUNTRY: U.S.A.

(F) ZIP: 20004

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/465,485

(B) FILING DATE: 05-JUN-1995

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/124,256

(B) FILING DATE: 20-SEP-1993

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/840,716

(B) FILING DATE: 21-FEB-1992

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/288,692

(B) FILING DATE: 22-DEC-1988

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Steven B. Kelber

(B) REGISTRATION NUMBER: 30,073

(C) REFERENCE/DOCKET NUMBER: 3335-075-55 CONT

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (202) 624-1200

(B) TELEFAX: (202) 624-1298

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(1) GENERAL INFORMATION:

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- (ii) TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
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 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
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- (A) APPLICATION NUMBER: US 08/465,485
 - (B) FILING DATE: 05-JUN-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 08/124,256
 - (B) FILING DATE: 20-SEP-1993
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- (A) APPLICATION NUMBER: US 07/840,716
 - (B) FILING DATE: 21-FEB-1992
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- (A) APPLICATION NUMBER: US 07/288,692
 - (B) FILING DATE: 22-DEC-1988
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Steven B. Kelber
 - (B) REGISTRATION NUMBER: 30,073
 - (C) REFERENCE/DOCKET NUMBER: 3335-075-55 CONT
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (202) 624-1200
 - (B) TELEFAX: (202) 624-1298

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGCGTGCGC CATCCTTCCC

20

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTTTTCCTCT GGGAAGGATG GCGCACGCTG GGAGA

35

(2) INFORMATION FOR SEQ ID NO:3:

- C1*
cont
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATGCACCTA CCCAGCCTCC

20

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACGGGGTACG GAGGCTGGGT AGGTGCATCT GGT

33

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACAAAGGCAT CCTGCAGTTG

20

(2) INFORMATION FOR SEQ ID NO:6:

- C1 Cont.*
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCCCAACTG CAGGATGCCT TTGTGGAAGT GTACGG

36

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGAAGGATG GCGCACGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

C CGTGCGAC CCTCTTG

17

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TACCGCGTGC GACCCTC

17

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TCCTACCGCG TCGGACC

17

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTTCCTACC GCGTGCG

17

(2) INFORMATION FOR SEQ ID NO:12:

- C1*
Cont
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACCCTTCCT ACCGCGT

17

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGACCCTT CCTACCG

17

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCGGCGGCAG CGCGG

15

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

C1 cont
(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGGCGGGGCG ACGGA

15

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGGAGCGCG GCGGGC

16

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCTCCCAGCG TGCGCCAT

18

(2) INFORMATION FOR SEQ ID NO:18:

- C1 Cont.*
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TGCACTCACG CTCGGCCT

18

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5086 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCGCCCGCCC CTCCGCGCCG CCTGCCCCGCC CGCCCGCCGC GCTCCCGCCC GCCGCTCTCC	60
GTGGCCCCCGC CGCGCTGCCG CCGCCGCCGC TGCCAGCGAA GGTGCCGGGG CTCCGGGCCC	120
TCCCTGCCGG CGGCCGTCAG CGCTCGGAGC GAACTGCGCG ACGGGAGGTC CGGGAGGCCA	180
CCGTAGTCGC GCCGCCGCGC AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG	240
GGGTGCGCCG GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGGAGAACTT CGTAGCAGTC	300
ATCCTTTTTA GGAAAAGAGG GAAAAAATAA AACCCTCCCC CACCACCTCC TTCTCCCCAC	360
CCCTCGCCGC ACCACACACA GCGCGGGCTT CTAGCGCTCG GCACCGGCGG GCCAGGCGCG	420
TCCTGCCTTC ATTTATCCAG CAGCTTTTCG GAAAATGCAT TTGCTGTTCG GAGTTTAATC	480
AGAAGACGAT TCCTGCCTCC GTCCCCGGCT CTTTCATCGT CCCATCTCCC CTGTCTCTCT	540
CCTGGGGAGG CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT	600
GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCGA ATACCGGACT	660
GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAAA AACTCGAGCT CTTGAGATCT	720
CCGGTTGGGA TTCCTGCGGA TTGACATTTC TGTGAAGCAG AAGTCTGGGA ATCGATCTGG	780
AAATCCTCCT AATTTTACT CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAAA	840
TCAGCTATAA CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG	900
GTTTTACAAA AAGGAAACTT GACAGAGGAT CATGCTGTAC TTAAAAAATA CAAGTAAGTC	960
TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC CTTTGAGATT TTTTACTTAA	1020
AGTGCAATTC AGTAAATTTA ATTTCCAGGC AGCTTAATAC ATTGTTTTTA GCCGTGTTAC	1080
TTGTAGTGTG TATGCCCTGC TTTCACTCAG TGTGTACAGG GAAACGCACC TGATTTTTTA	1140
CTTATTAGTT TGTTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA	1200
CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA TTGGAATAAA	1260
AATTCCTGC GTCTCATGCC AAGAGGGAAA CACCAGAATC AAGTGTTCCG CGTGATTGAA	1320
GACACCCCCT CGTCCAAGAA TGCAAAGCAC ATCCAATAAA ATAGCTGGAT TATAACTCCT	1380
CTTCTTTCTC TGGGGGCCGT GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCCGTT	1440
GCTTTTCCTC TGGGAAGGAT GGCGCACGCT GGGAGAACGG GGTACGACAA CCGGGAGATA	1500
GTGATGAAGT ACATCCATTA TAAGCTGTCG CAGAGGGGCT ACGAGTGGGA TGCGGGAGAT	1560
GTGGGCGCCG CGCCCCCGGG GGCCGCCCCC GCACCGGGCA TCTTCTCCTC CCAGCCCGGG	1620
CACACGCCCC ATCCAGCCGC ATCCCGCGAC CCGGTCGCCA GGACCTCGCC GCTGCAGACC	1680

CCGGCTGCCC	CCGGCGCCGC	CGCGGGGCCT	GCGCTCAGCC	CGGTGCCACC	TGTGGTCCAC	1740
CTGGCCCTCC	GCCAAGCCGG	CGACGACTTC	TCCCGCCGCT	ACCGCGGCGA	CTTCGCCGAG	1800
ATGTCCAGCC	AGCTGCACCT	GACGCCCTTC	ACCGCGCGGG	GACGCTTTGC	CACGGTGGTG	1860
GAGGAGCTCT	TCAGGGACGG	GGTGAAGTGG	GGGAGGATTG	TGGCCTTCTT	TGAGTTCGGT	1920
GGGGTCATGT	GTGTGGAGAG	CGTCAACCGG	GAGATGTCGC	CCCTGGTGGA	CAACATCGCC	1980
CTGTGGATGA	CTGAGTACCT	GAACCGGCAC	CTGCACACCT	GGATCCAGGA	TAACGGAGGC	2040
TGGGATGCCT	TTGTGGAACT	GTACGGCCCC	AGCATGCGGC	CTCTGTTTGA	TTTCTCCTGG	2100
CTGTCTCTGA	AGACTCTGCT	CAGTTTGGCC	CTGGTGGGAG	CTTGCATCAC	CCTGGGTGCC	2160
TATCTGAGCC	ACAAGTGAAG	TCAACATGCC	TGCCCCAAAC	AAATATGCAA	AAGGTTCACT	2220
AAAGCAGTAG	AAATAATATG	CATTGTCAGT	GATGTACCAT	GAAACAAAGC	TGCAGGCTGT	2280
TTAAGAAAAA	ATAACACACA	TATAAACATC	ACACACACAG	ACAGACACAC	ACACACACAA	2340
CAATTAACAG	TCTTCAGGCA	AAACGTCGAA	TCAGCTATTT	ACTGCCAAAG	GGAAATATCA	2400
TTTATTTTTT	ACATTATTAA	GAAAAAAGAT	TTATTTATTT	AAGACAGTCC	CATCAAAACT	2460
CCGTCTTTGG	AAATCCGACC	ACTAATTGCC	AAACACCGCT	TCGTGTGGCT	CCACCTGGAT	2520
GTTCTGTGCC	TGTAAACATA	GATTCGCTTT	CCATGTTGTT	GGCCGGATCA	CCATCTGAAG	2580
AGCAGACGGA	TGGAAAAAGG	ACCTGATCAT	TGGGGAAGCT	GGCTTTCTGG	CTGCTGGAGG	2640
CTGGGGAGAA	GGTGTTTCATT	CACTTGCATT	TCTTTGCCCT	GGGGGCGTGA	TATTAACAGA	2700
GGGAGGGTTC	CCGTGGGGGG	AAGTCCATGC	CTCCCTGGCC	TGAAGAAGAG	ACTCTTTGCA	2760
TATGACTCAC	ATGATGCATA	CCTGGTGGGA	GGAAAAGAGT	TGGGAACTTC	AGATGGACCT	2820
AGTACCCACT	GAGATTTCCA	CGCCGAAGGA	CAGCGATGGG	AAAAATGCCC	TTAAATCATA	2880
GGAAAGTATT	TTTTTAAGCT	ACCAATTGTG	CCGAGAAAAG	CATTTTAGCA	ATTTATACAA	2940
TATCATCCAG	TACCTTAAAC	CCTGATTGTG	TATATTCATA	TATTTTGGAT	ACGCACCCCC	3000
CAACTCCCAA	TACTGGCTCT	GTCTGAGTAA	GAAACAGAAT	CCTCTGGAAC	TTGAGGAAGT	3060
GAACATTTCT	GTGACTTCCG	ATCAGGAAGG	CTAGAGTTAC	CCAGAGCATC	AGGCCGCCAC	3120
AAGTGCCTGC	TTTTAGGAGA	CCGAAGTCCG	CAGAACCTAC	CTGTGTCCCA	GCTTGGAGGC	3180
CTGGTCCTGG	AACTGAGCCG	GGCCCTCACT	GGCCTCCTCC	AGGGATGATC	AACAGGGTAG	3240
TGTGGTCTCC	GAATGTCTGG	AAGCTGATGG	ATGGAGCTCA	GAATTCCACT	GTCAAGAAAG	3300
AGCAGTAGAG	GGGTGTGGCT	GGGCCTGTCA	CCCTGGGGCC	CTCCAGGTAG	GCCCGTTTTT	3360
ACGTGGAGCA	TAGGAGCCAC	GACCCTTCTT	AAGACATGTA	TCACTGTAGA	GGGAAGGAAC	3420

AGAGGCCCTG	GGCCTTCCTA	TCAGAAGGAC	ATGGTGAAGG	CTGGGAACGT	GAGGAGAGGC	3480
AATGGCCACG	CCCCATTTTG	GCTGTAGCAC	ATGGCACGTT	GGCTGTGTGG	CCTTGGCCAC	3540
CTGTGAGTTT	AAAGCAAGGC	TTTAAATGAC	TTTGGAGAGG	GTCACAAATC	CTAAAAGAAG	3600
CATTGAAGTG	AGGTGTCATG	GATTAATTGA	CCCCTGTCTA	TGGAATTACA	TGTAAAACAT	3660
TATCTTGTC	CTGTAGTTTG	GTTTTATTTG	AAAACCTGAC	AAAAAAAAAG	TTCCAGGTGT	3720
GGAATATGGG	GGTTATCTGT	ACATCCTGGG	GCATTAAAAA	AAAATCAATG	GTGGGGAAC	3780
ATAAAGAAGT	AACAAAAGAA	GTGACATCTT	CAGCAAATAA	ACTAGGAAAT	TTTTTTTTCT	3840
TCCAGTTTAG	AATCAGCCTT	GAAACATTGA	TGGAATAACT	CTGTGGCATT	ATTGCATTAT	3900
ATACCATTTA	TCTGTATTAA	CTTTGGAATG	TACTCTGTTC	AATGTTTAAT	GCTGTGGTTG	3960
ATATTTGAA	AGCTGCTTTA	AAAAAATACA	TGCATCTCAG	CGTTTTTTTG	TTTTTAATTG	4020
TATTTAGTTA	TGGCCTATAC	ACTATTTGTG	AGCAAAGGTG	ATCGTTTTCT	GTTTGAGATT	4080
TTTATCTCTT	GATTCTTCAA	AAGCATTCTG	AGAAGGTGAG	ATAAGCCCTG	AGTCTCAGCT	4140
ACCTAAGAAA	AACCTGGATG	TCACTGGCCA	CTGAGGAGCT	TTGTTTCAAC	CAAGTCATGT	4200
GCATTTCCAC	GTCAACAGAA	TTGTTTATTG	TGACAGTTAT	ATCTGTTGTC	CCTTTGACCT	4260
TGTTTCTTGA	AGGTTTCCTC	GTCCCTGGGC	AATTCCGCAT	TTAATTCATG	GTATTCAGGA	4320
TACATGCAT	GTTTGTTTAA	ACCCATGAGA	TTCATTCACT	TAAAAATCCA	GATGGCGAAT	4380
GACCAGCAGA	TTCAAATCTA	TGGTGGTTTG	ACCTTTAGAG	AGTTGCTTTA	CGTGGCCTGT	4440
TTCAACACAG	ACCCACCCAG	AGCCCTCCTG	CCCTCCTTCC	GCGGGGGCTT	TCTCATGGCT	4500
GTCCTTCAGG	GTCTTCCTGA	AATGCAGTGG	TCGTTACGCT	CCACCAAGAA	AGCAGGAAAC	4560
CTGTGGTATG	AAGCCAGACC	TCCCCGGCGG	GCCTCAGGGA	ACAGAATGAT	CAGACCTTTG	4620
AATGATTCTA	ATTTTAAAGC	AAAATATTAT	TTTATGAAAG	GTTTACATTG	TCAAAGTGAT	4680
GAATATGGAA	TATCCAATCC	TGTGCTGCTA	TCCTGCCAAA	ATCATTTTAA	TGGAGTCAGT	4740
TTGCAGTATG	CTCCACGTGG	TAAGATCCTC	CAAGCTGCTT	TAGAAGTAAC	AATGAAGAAC	4800
GTGGACGTTT	TTAATATAAA	GCCTGTTTTG	TCTTTTGTTG	TTGTTCAAAC	GGGATTCACA	4860
GAGTATTTGA	AAAATGTATA	TATATTAAGA	GGTCACGGGG	GCTAATTGCT	AGCTGGCTGC	4920
CTTTTGCTGT	GGGGTTTTGT	TACCTGGTTT	TAATAACAGT	AAATGTGCCC	AGCCTCTTGG	4980
CCCCAGAACT	GTACAGTATT	GTGGCTGCAC	TTGCTCTAAG	AGTAGTTGAT	GTTGCATTTT	5040
CCTTATTGTT	AAAAACATGT	TAGAAGCAAT	GAATGTATAT	AAAAGC		5086

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC CGG GAG ATA GTG ATG	48
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met	
1 5 10 15	
AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC TAC GAG TGG GAT GCG	96
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala	
20 25 30	
GGA GAT GTG GGC GCC GCG CCC CCG GGG GCC GCC CCC GCA CCG GGC ATC	144
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile	
35 40 45	
TTC TCC TCC CAG CCC GGG CAC ACG CCC CAT CCA GCC GCA TCC CGC GAC	192
Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp	
50 55 60	
CCG GTC GCC AGG ACC TCG CCG CTG CAG ACC CCG GCT GCC CCC GGC GCC	240
Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala	
65 70 75 80	
GCC GCG GGG CCT GCG CTC AGC CCG GTG CCA CCT GTG GTC CAC CTG GCC	288
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala	
85 90 95	
CTC CGC CAA GCC GGC GAC GAC TTC TCC CGC CGC TAC CGC GGC GAC TTC	336
Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe	
100 105 110	
GCC GAG ATG TCC AGC CAG CTG CAC CTG ACG CCC TTC ACC GCG CGG GGA	384
Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly	
115 120 125	
CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG GAC GGG GTG AAC TGG	432
Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp	
130 135 140	
GGG AGG ATT GTG GCC TTC TTT GAG TTC GGT GGG GTC ATG TGT GTG GAG	480
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu	
145 150 155 160	

AGC	GTC	AAC	CGG	GAG	ATG	TCG	CCC	CTG	GTG	GAC	AAC	ATC	GCC	CTG	TGG	528
Ser	Val	Asn	Arg	Glu	Met	Ser	Pro	Leu	Val	Asp	Asn	Ile	Ala	Leu	Trp	
			165						170					175		
ATG	ACT	GAG	TAC	CTG	AAC	CGG	CAC	CTG	CAC	ACC	TGG	ATC	CAG	GAT	AAC	576
Met	Thr	Glu	Tyr	Leu	Asn	Arg	His	Leu	His	Thr	Trp	Ile	Gln	Asp	Asn	
			180					185					190			
GGA	GGC	TGG	GAT	GCC	TTT	GTG	GAA	CTG	TAC	GGC	CCC	AGC	ATG	CGG	CCT	624
Gly	Gly	Trp	Asp	Ala	Phe	Val	Glu	Leu	Tyr	Gly	Pro	Ser	Met	Arg	Pro	
		195					200					205				
CTG	TTT	GAT	TTC	TCC	TGG	CTG	TCT	CTG	AAG	ACT	CTG	CTC	AGT	TTG	GCC	672
Leu	Phe	Asp	Phe	Ser	Trp	Leu	Ser	Leu	Lys	Thr	Leu	Leu	Ser	Leu	Ala	
	210					215					220					
CTG	GTG	GGA	GCT	TGC	ATC	ACC	CTG	GGT	GCC	TAT	CTG	AGC	CAC	AAG		717
Leu	Val	Gly	Ala	Cys	Ile	Thr	Leu	Gly	Ala	Tyr	Leu	Ser	His	Lys		
225					230					235						

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Ala	His	Ala	Gly	Arg	Thr	Gly	Tyr	Asp	Asn	Arg	Glu	Ile	Val	Met
1				5					10					15	
Lys	Tyr	Ile	His	Tyr	Lys	Leu	Ser	Gln	Arg	Gly	Tyr	Glu	Trp	Asp	Ala
		20						25					30		
Gly	Asp	Val	Gly	Ala	Ala	Pro	Pro	Gly	Ala	Ala	Pro	Ala	Pro	Gly	Ile
	35					40					45				
Phe	Ser	Ser	Gln	Pro	Gly	His	Thr	Pro	His	Pro	Ala	Ala	Ser	Arg	Asp
	50				55					60					
Pro	Val	Ala	Arg	Thr	Ser	Pro	Leu	Gln	Thr	Pro	Ala	Ala	Pro	Gly	Ala
65					70				75					80	
Ala	Ala	Gly	Pro	Ala	Leu	Ser	Pro	Val	Pro	Pro	Val	Val	His	Leu	Ala
			85					90					95		
Leu	Arg	Gln	Ala	Gly	Asp	Asp	Phe	Ser	Arg	Arg	Tyr	Arg	Gly	Asp	Phe
		100					105						110		
Ala	Glu	Met	Ser	Ser	Gln	Leu	His	Leu	Thr	Pro	Phe	Thr	Ala	Arg	Gly
	115					120						125			
Arg	Phe	Ala	Thr	Val	Val	Glu	Glu	Leu	Phe	Arg	Asp	Gly	Val	Asn	Trp
	130					135					140				

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
 145 150 155 160
 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
 165 170 175
 Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
 180 185 190
 Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
 195 200 205
 Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
 210 215 220
 Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Ser His Lys
 225 230 235

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC CGG GAG ATA GTG ATG	48
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met	
1 5 10 15	
AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC TAC GAG TGG GAT GCG	96
Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala	
20 25 30	
GGA GAT GTG GGC GCC GCG CCC CCG GGG GCC GCC CCC GCA CCG GGC ATC	144
Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile	
35 40 45	
TTC TCC TCC CAG CCC GGG CAC ACG CCC CAT CCA GCC GCA TCC CGC GAC	192
Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp	
50 55 60	
CCG GTC GCC AGG ACC TCG CCG CTG CAG ACC CCG GCT GCC CCC GGC GCC	240
Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala	
65 70 75 80	

GCC GCG GGG CCT GCG CTC AGC CCG GTG CCA CCT GTG GTC CAC CTG GCC	288
Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala	
85 90 95	
CTC CGC CAA GCC GGC GAC GAC TTC TCC CGC CGC TAC CGC GGC GAC TTC	336
Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe	
100 105 110	
GCC GAG ATG TCC AGC CAG CTG CAC CTG ACG CCC TTC ACC GCG CGG GGA	384
Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly	
115 120 125	
CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG GAC GGG GTG AAC TGG	432
Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp	
130 135 140	
GGG AGG ATT GTG GCC TTC TTT GAG TTC GGT GGG GTC ATG TGT GTG GAG	480
Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu	
145 150 155 160	
AGC GTC AAC CGG GAG ATG TCG CCC CTG GTG GAC AAC ATC GCC CTG TGG	528
Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp	
165 170 175	
ATG ACT GAG TAC CTG AAC CGG CAC CTG CAC ACC TGG ATC CAG GAT AAC	576
Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn	
180 185 190	
GGA GGC TGG GTA GGT GCA TCT GGT GAT GTG AGT CTG GGC	615
Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly	
195 200 205	

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn Arg Glu Ile Val Met
 1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
 20 25 30

Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Ile
 35 40 45

Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60

Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80

Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Ala
85 90 95

Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Gly Asp Phe
100 105 110

Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
115 120 125

Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
130 135 140

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145 150 155 160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
165 170 175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
180 185 190

Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly
195 200 205

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;
(A) DESCRIPTION: Synthetic DNA

(iv) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: Modified_base
- (B) LOCATION: 16..17
- (D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TCTCCCAGCG TGCGCCAT

18

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

(A) DESCRIPTION: Synthetic DNA

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: Modified_base

(B) LOCATION: 16..17

(D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGCACTCACG CTCGGCCT

18

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

(A) DESCRIPTION: Synthetic DNA

(iv) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: Modified_base

(B) LOCATION: 18..19

(D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCGCGGCGGG CGGGCGGGCA

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

(A) DESCRIPTION: Synthetic DNA

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: Modified_base

(B) LOCATION: 18..19

(D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGGCGGAGGC CGGCCGGCGG

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

(A) DESCRIPTION: Synthetic DNA

(iv) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: Modified_base
- (B) LOCATION: 18..19
- (D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCGGCGGCG GCGGCAGCGC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid;

(A) DESCRIPTION: Synthetic DNA

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: Modified_base
- (B) LOCATION: 18..19
- (D) OTHER INFORMATION: Last two internucleoside linkages are phosphorothioates

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGCCGGGAA GGGCGCCCGC

20